FIG. 1A	FIG. 1B
FIG. 1C	FIG. 1D

FIG. 1

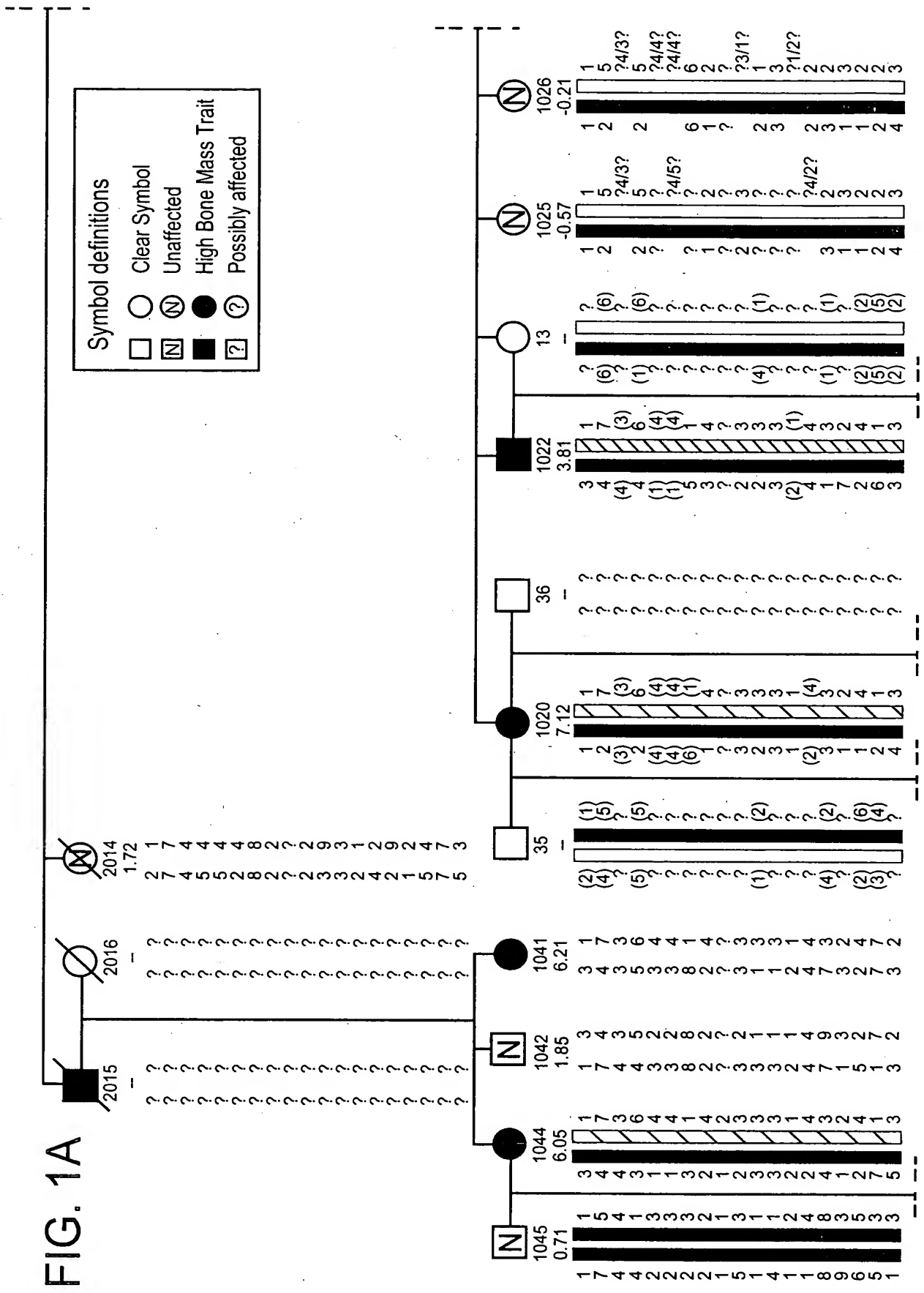
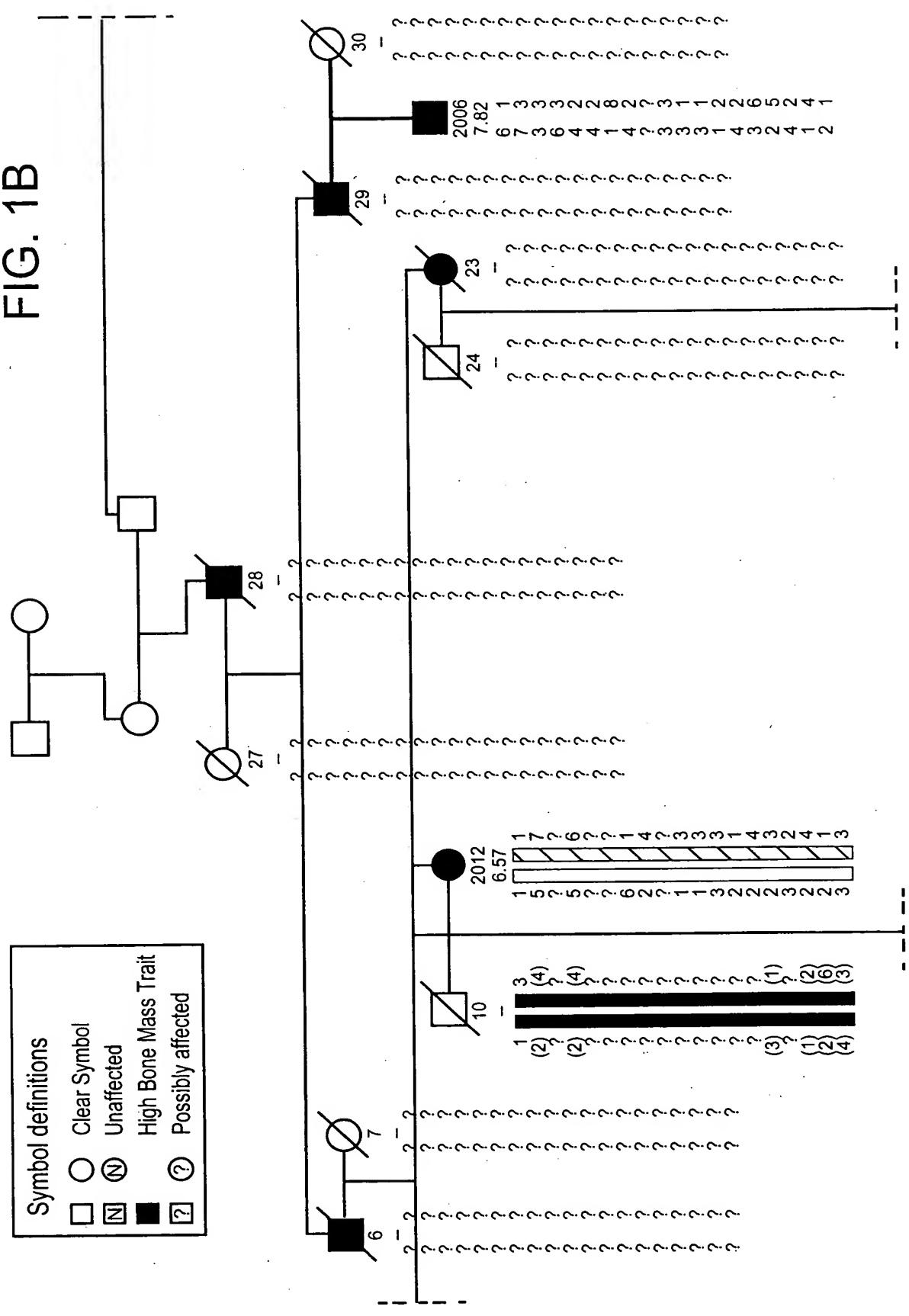
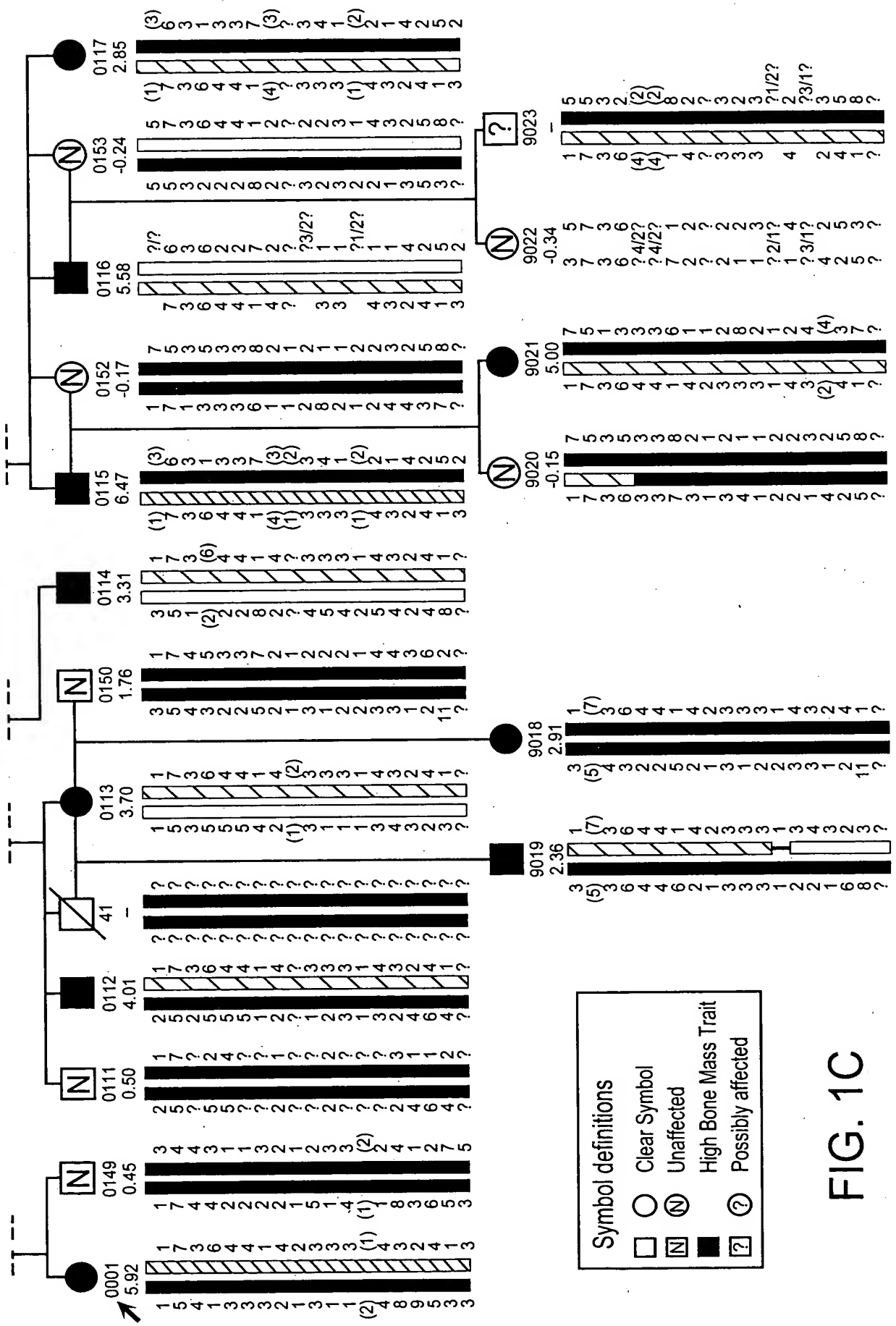

Symbol definitions
Clear Symbol
Unaffected
High Bone Mass Trait
Possibly affected
2014
1.72
2016
2015
1041
6.21
1042
1.85
1044
6.05
1045
0.71
1020
7.12
1022
3.81
1025
-0.57
1026
-0.21
13
35
36

FIG. 1A

FIG. 1B


Symbol definitions
Clear Symbol
Unaffected
High Bone Mass Trait
Possibly affected
30
2006
7.82
29
23
24
28
27
2012
6.57
10
7
6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5.92
0149
0.45
0111
0.50
0112
4.01
41
0113
3.70
0150
1.76
0114
3.31
0115
6.47
0152
-0.17
0116
5.58
0153
-0.24
0117
2.85
9019
2.36
9018
2.91
9020
-0.15
9021
5.00
9022
-0.34
9023
Symbol definitions
Clear Symbol
Unaffected
High Bone Mass Trait
Possibly affected

FIG. 1C

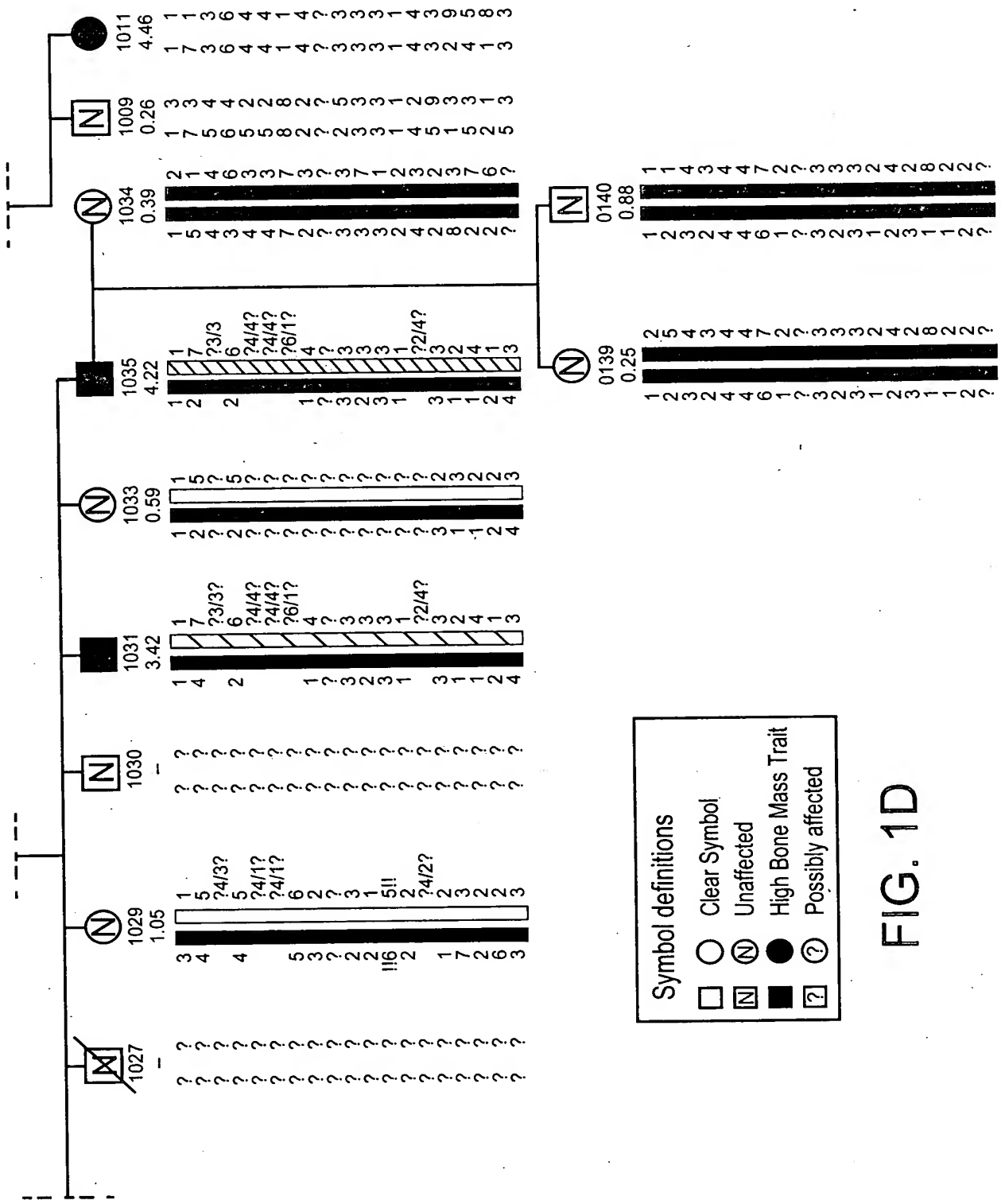

1011
4.46
1009
0.26
1034
0.39
1035
4.22
1033
0.59
1031
3.42
1030
1029
1.05
1027
0140
0.88
0139
0.25
Symbol definitions
Clear Symbol
Unaffected
High Bone Mass Trait
Possibly affected

FIG. 1D

FIG. 2A

BAC/STS Map of the HBM Region

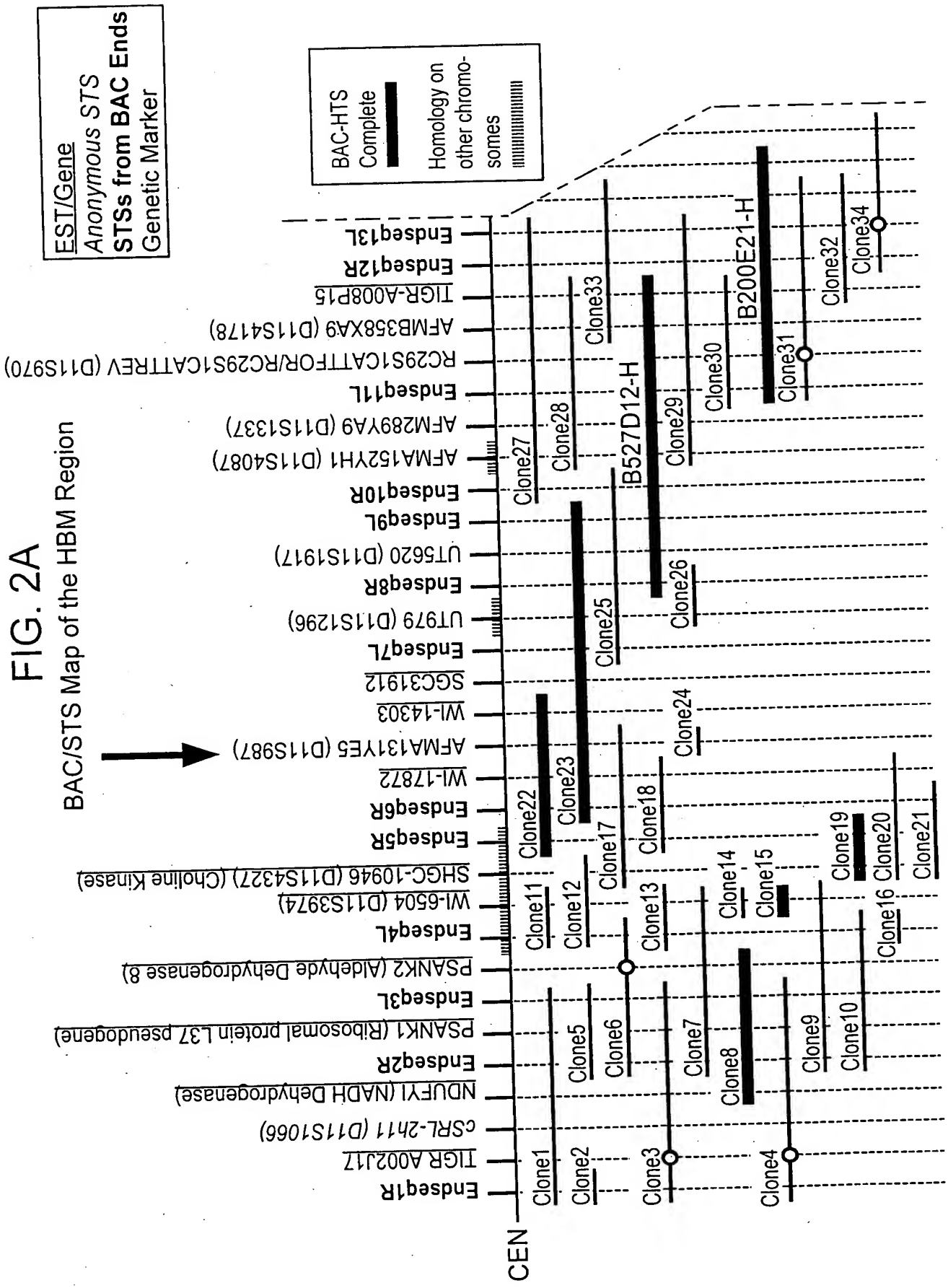
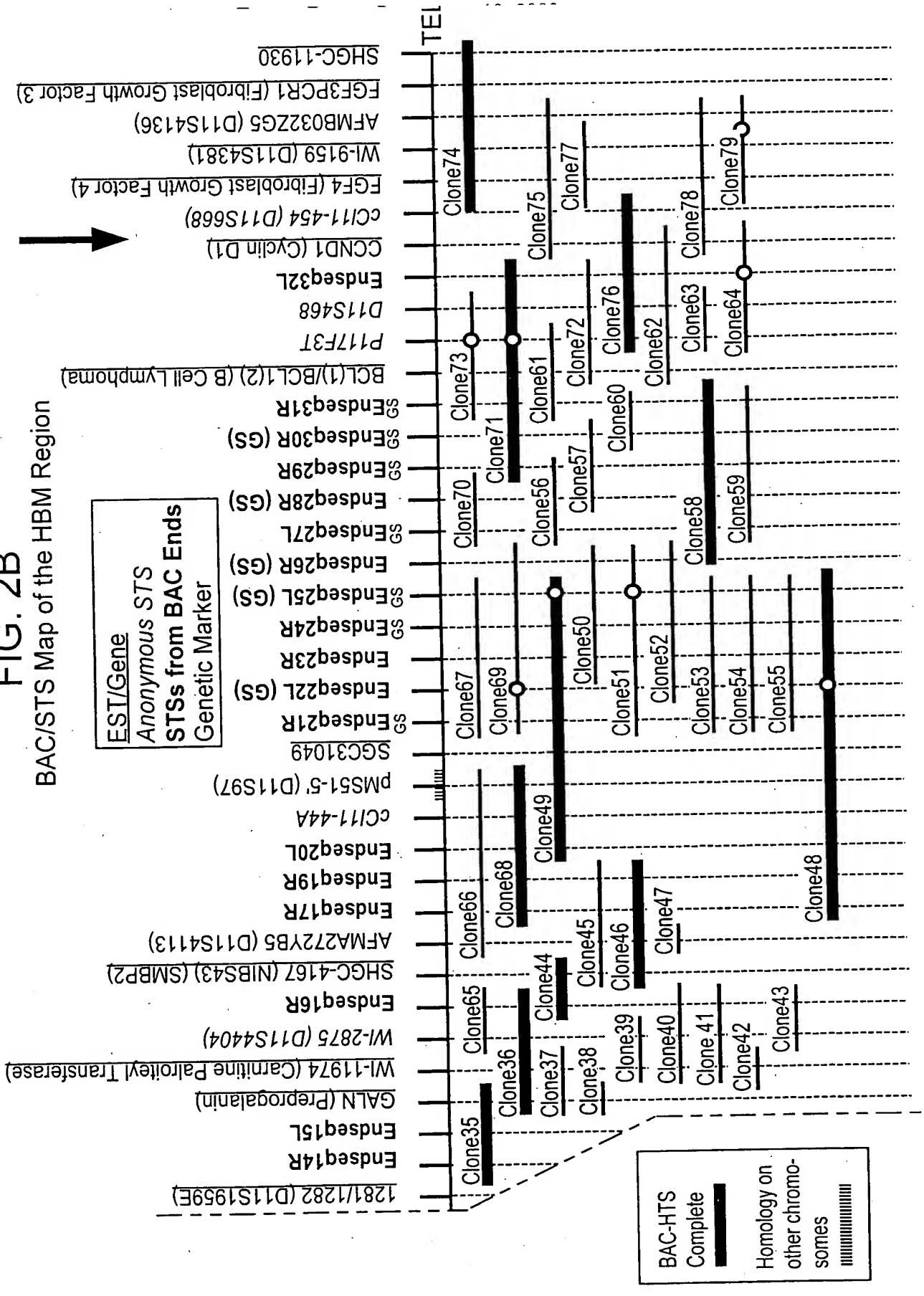


FIG. 2B
BAC/STS Map of the HBM Region



Exon 1
ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCG
GGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCGCCGCCCGGGCCG
CCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC
TGCCCGGCCCCCGCCGCGGCC

Exon 2 Coordinates: 527d12_Contig308G 30944-30549
gccccacagCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGC
TGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGC
GGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGC
CGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCT
GAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGG
TCTCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACT
GGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGC
ACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCC
ATCGCCTTGGACCCCGCTCACGGgtaaaccctgctg

... 9408 nt ...

Exon 3 Coordinates: 527d12_Contig308G 21141-20945
ccccgtcacagGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTG
AGCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCG
GACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAG
CTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG
GACGGCTCGTTCCGgtaggtacccac

... 6094 nt ...

Exon 4 Coordinates: 527d12_Contig308G 15047-14850
tccctgactgcagGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCC
CTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGC
TCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGAT
CCTGAGTGCCCTATACTCACCCATGGACATCCAGGTGCTGAGCCAGGA
GCGGCAGCCTTTCTgtgagtgccgg

... 1827 nt ...

Exon 5 Coordinates: 527d12_Contig308G 13220-13088
tttctcagTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTG
TGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACG
GGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGgtgaggcggtgg
gacg

FIG. 3A

... 20923 nt ...

Exon 6 Coordinates: 527d12_Contig309G 7705-8100
ctccacag**GAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTAC**
GGAGGATCTCGCTGGACACGCCGGACTTCACCGACATCGTGCTGCAGG
TGGACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGG
GCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCG
TACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAA
CGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTG
GACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCA
CCTCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCC
ATCGCACTGCACCCCGTGATGGGgtaagacgggc

..... 3211 nt .....

Exon 7 Coordinates: 527d12_Contig309G 11311-11482
ttcttctccag**CCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGA**
GTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTC
CCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGC
TCTACTGGGGAGACGCCAAGACAGACAAGATCGAGgtgaggctcctgtgg

..... 13445 nt .....

Exon 8 Coordinates: 527d12_Contig309G 24927-25143
ccgtcctgcag**GTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGA**
GGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCAT
CTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGG
TCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGG
GGCTCAAAGCTGTGAATGTGGCCAAGGTCGTCGgtgagtccgggggggtc

....2826 nt .....

Exon 9 Coordinates: 527d12_Contig309G 27969-28256
gttcgcttccag**GAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCA**
CCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGG
CCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTT
CTTGGTCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGAC
CAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGCCTC
AGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGT
CAGCCTGAAGgtagcgtgggc

.....3102.....

FIG. 3B

Exon 10 Coordinates: 527d12_Contig309G 31358-31582
cctgctgccagACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCA
CGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTG
GATGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGA
AGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTGGAGGG
ACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGgtaagtgtt
tgcctgtc

.....1297 nt.....

Exon 11 Coordinates: 527d12_Contig309G 32879-33064
gtgccttccagCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCG
TGCGGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAG
GTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCGCCTC
TACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTG
Ggtgagggccgggct

.....2069 nt.....

Exon 12 Coordinates: 527d12_Contig309G 35133-35454
gtgttcatgcagGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCG
TTCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAAT
CTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCAC
CCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCA
CTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCA
GTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCT
GCGCCTCACACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCgtaag
tgcctcatggt

.....2006 nt.....

Exon 13 Coordinates: 527d12_Contig309G 37460-37659
gcctcctctaCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG
TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCT
GCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAA
GTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGA
CGACGGGACCCAGgcaggtgccctgtgg

.....6965 nt.....

FIG. 3C

Exon 14 Coordinates: 527d12_Contig309G 44624-44832
ctttgtcttacagCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGAC
AGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTC
TGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGG
GGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGG
CCATCGTCGTCAACGCGGAGCGAGGgtaggaggccaac

.....1404 nt.....

Exon 15 Coordinates: 527d12_Contig309G 46236-46427
ccaccctcccgcagGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAA
GATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCA
CCACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGG
GCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGT
GACCTGTCAGgtacgcgccccgg

.....686 nt.....

Exon 16 Coordinates: 527d12_Contig309G 47113-47322
ggctgcttgcagGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCA
GCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCG
CCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGC
GGACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAG
TGGAGGAAGTCAGCCTGGAGGAGTTCTgtacgtgggggc

.....3884 nt.....

Exon 17 Coordinates: 527d12_Contig309G 51206-51331
ttgtctttgcagCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACA
TCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCC
ACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGgtaggtgtgacctaggtgc

....3905 nt.....

Exon 18 Coordinates: 527d12_Contig309G 55236-55472
gttctcctctgtccctcccccagAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGT
GCCACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGG
CTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGT
GCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGC
GCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAG
GTGGACTGTGACGgtgaggccctcc

.....3052 nt.....

FIG. 3D

Exon 19 Coordinates: 527d12_Contig309G 58524-58634
tctccttgcagCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGT
GTGTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACG
GCTCCGACGAGCTCATGTGTGgtgagccagctt

.....1448 nt.....

Exon 20 Coordinates: 527d12_Contig309G 60082-60319
gtttgtctctggcagAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACA
GCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCAT
GGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGC
GGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGC
ACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCT
TCACAGgtaaggagcctgagatatggaa

....1095 nt.....

Exon 21 Coordinates: 527d12_Contig309G 61414-61552
cttccctgccagGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTG
ATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCACGTCAC
AGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCC
GCCGgtgaggggcggg

.....6513 nt.....

Exon 22 Coordinates: 527d12_Contig309G 68065-68162
ttggctctcctcagATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCC
TGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGA
GACCGTACAGgtaggacatcccctgcag

.....2273 nt.....

FIG. 3E

Exon 23 Coordinates: 527d12_Contig309G 70435-70901

tcaaacattccggccactgcgagaccgtacagGCCCTACATCATTCGAGGAATGGCGCCCC
CGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCC
AGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCA
GACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCG
GAGGACAGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCAT
CTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACCTCGGC
CGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAA
AGAAAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAA
AAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTT
TGTACAGTGGAGAAATATTTATAAACTTAATTTTGTAAAACA

FIG. 3F

Model for a LDL Receptor-Related protein, Zmax1

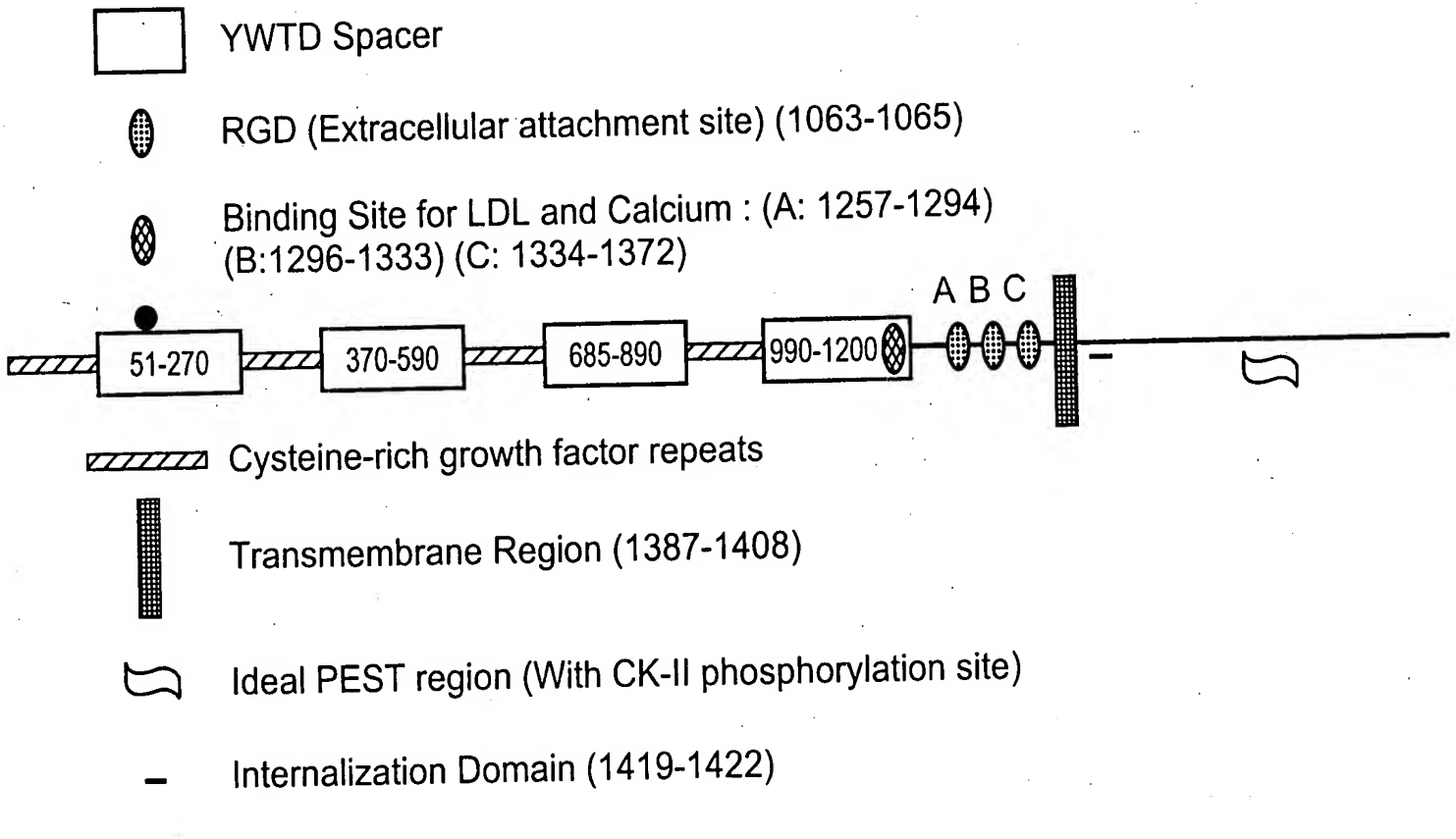


FIG. 4

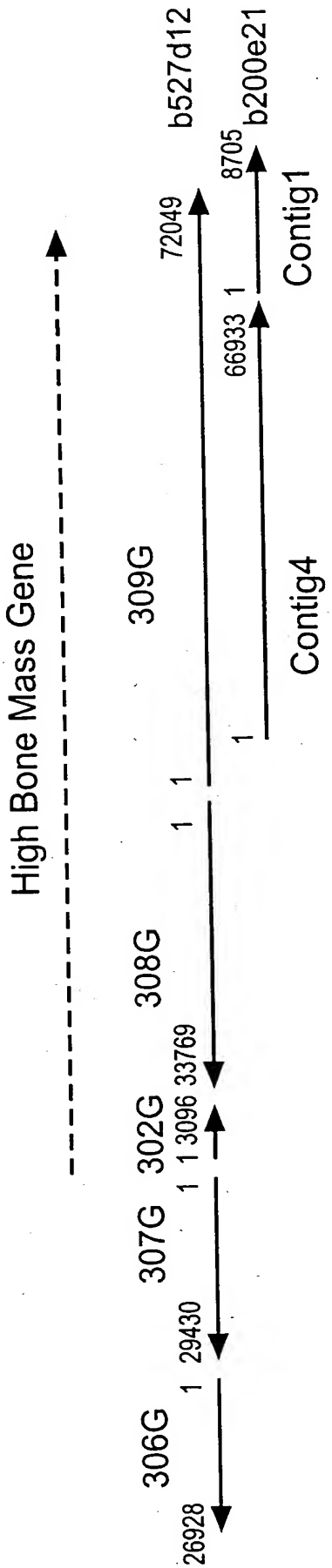
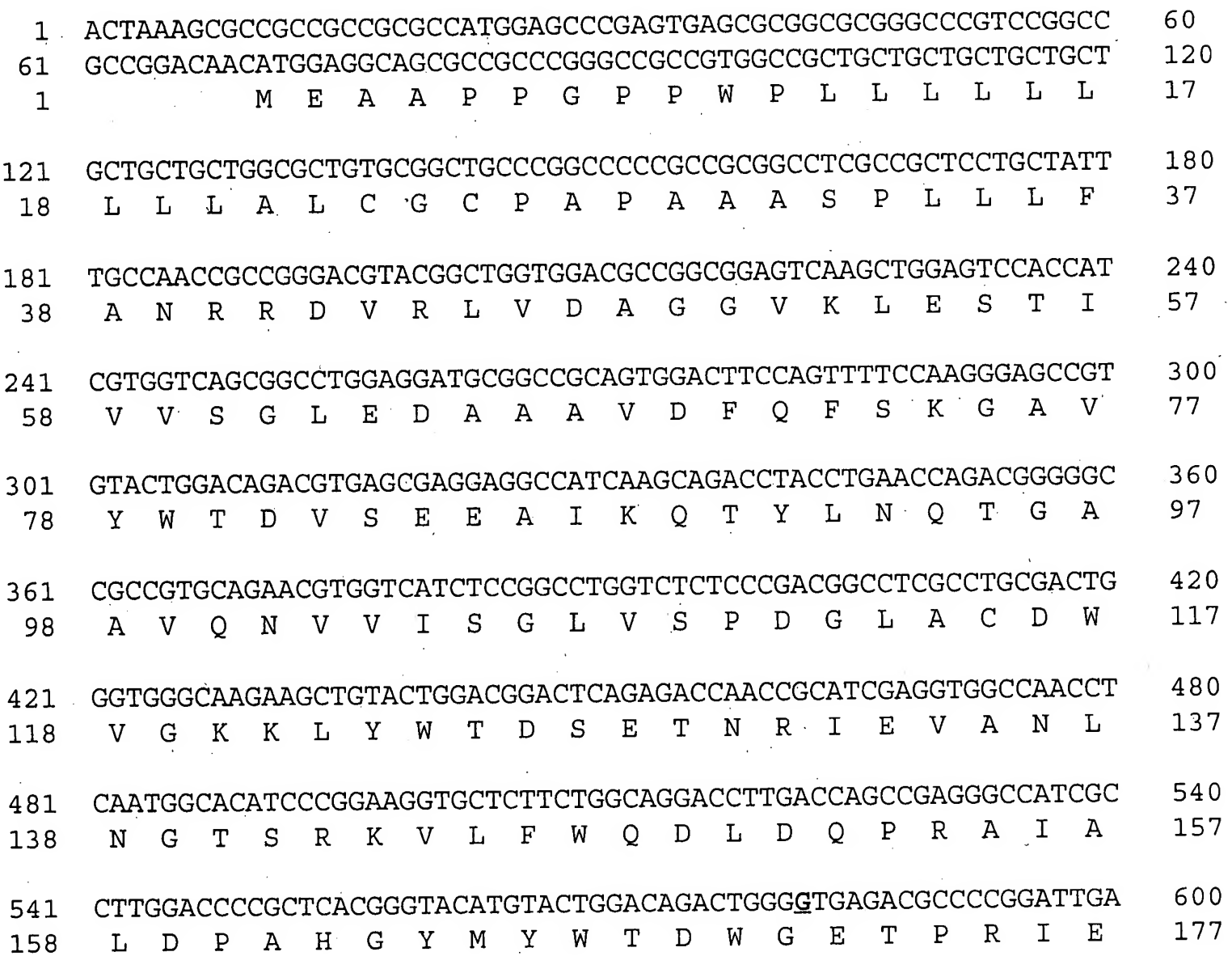

High Bone Mass Gene
306G
1
29430
26928
307G
1
1 3096
302G
1
33769
308G
1
309G
1
72049
b527d12
Contig4
1
66933
1
8705
b200e21
Contig1

FIG. 5

FIG. 6A



APPLN. FILING DATE: DECEMBER 10, 2003
TITLE: HIGH BONE MASS GENE OF 11Q13.3
INVENTOR(S): JOHN P. CARULLI ET AL.
ATTORNEY'S DOCKET NO: 032796-217 SHEET 16 of 32

FIG. 6B

```
601  GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC  660
178   R  A  G  M  D  G  S  T  R  K  I  I  V  D  S  D  I  Y  W  P   197

661  CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG  720
198   N  G  L  T  I  D  L  E  E  Q  K  L  Y  W  A  D  A  K  L  S   217

721  CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT  780
218   F  I  H  R  A  N  L  D  G  S  F  R  Q  K  V  V  E  G  S  L   237

781  GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC  840
238   T  H  P  F  A  L  T  L  S  G  D  T  L  Y  W  T  D  W  Q  T   257

841  CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC  900
258   R  S  I  H  A  C  N  K  R  T  G  G  K  R  K  E  I  L  S  A   277

901  CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC  960
278   L  Y  S  P  M  D  I  Q  V  L  S  Q  E  R  Q  P  F  F  H  T   297

961  TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC  1020
298   R  C  E  E  D  N  G  G  C  S  H  L  C  L  L  S  P  S  E  P   317

1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA  1080
318   F  Y  T  C  A  C  P  T  G  V  Q  L  Q  D  N  G  R  T  C  K   337

1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT  1140
338   A  G  A  E  E  V  L  L  L  A  R  R  T  D  L  R  R  I  S  L   357
```

APPLN. FILING DATE: DECEMBER 10, 2003
TITLE: HIGH BONE MASS GENE OF 11Q13.3
INVENTOR(S): JOHN P. CARULLI ET AL.
ATTORNEY'S DOCKET NO: 032796-217 SHEET 17 of 32

FIG. 6C

```
1141  GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC   1200
 358   D  T  P  D  F  T  D  I  V  L  Q  V  D  D  I  R  H  A  I  A    377

1201  CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT   1260
 378   I  D  Y  D  P  L  E  G  Y  V  Y  W  T  D  D  E  V  R  A  I    397

1261  CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA   1320
 398   R  R  A  Y  L  D  G  S  G  A  Q  T  L  V  N  T  E  I  N  D    417

1321  CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC   1380
 418   P  D  G  I  A  V  D  W  V  A  R  N  L  Y  W  T  D  T  G  T    437

1381  GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA   1440
 438   D  R  I  E  V  T  R  L  N  G  T  S  R  K  I  L  V  S  E  D    457

1441  CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA   1500
 458   L  D  E  P  R  A  I  A  L  H  P  V  M  G  L  M  Y  W  T  D    477

1501  CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT   1560
 478   W  G  E  N  P  K  I  E  C  A  N  L  D  G  Q  E  R  R  V  L    497

1561  GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT   1620
 498   V  N  A  S  L  G  W  P  N  G  L  A  L  D  L  Q  E  G  K  L    517

1621  CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG   1680
 518   Y  W  G  D  A  K  T  D  K  I  E  V  I  N  V  D  G  T  K  R    537
```

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TITLE: HIGH BONE MASS GENE OF 11Q13.3
INVENTOR(S): JOHN P. CARULLI ET AL.
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FIG. 6D

```
1681  GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT  1740
 538   R  T  L  L  E  D  K  L  P  H  I  F  G  F  T  L  L  G  D  F   557

1741  CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG  1800
 558   I  Y  W  T  D  W  Q  R  R  S  I  E  R  V  H  K  V  K  A  S   577

1801  CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC  1860
 578   R  D  V  I  I  D  Q  L  P  D  L  M  G  L  K  A  V  N  V  A   597

1861  CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT  1920
 598   K  V  V  G  T  N  P  C  A  D  R  N  G  G  C  S  H  L  C  F   617

1921  CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT  1980
 618   F  T  P  H  A  T  R  C  G  C  P  I  G  L  E  L  L  S  D  M   637

1981  GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG  2040
 638   K  T  C  I  V  P  E  A  F  L  V  F  T  S  R  A  A  I  H  R   657

2041  GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC  2100
 658   I  S  L  E  T  N  N  N  D  V  A  I  P  L  T  G  V  K  E  A   677

2101  CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA  2160
 678   S  A  L  D  F  D  V  S  N  N  H  I  Y  W  T  D  V  S  L  K   697

2161  GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT  2220
 698   T  I  S  R  A  F  M  N  G  S  S  V  E  H  V  V  E  F  G  L   717
```

APPLN. FILING DATE: DECEMBER 10, 2003
TITLE: HIGH BONE MASS GENE OF 11Q13.3
INVENTOR(S): JOHN P. CARULLI ET AL.
ATTORNEY'S DOCKET NO: 032796-217

FIG. 6E

```
2221  TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC  2280
 718   D  Y  P  E  G  M  A  V  D  W  M  G  K  N  L  Y  W  A  D  T    737

2281  TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG  2340
 738   G  T  N  R  I  E  V  A  R  L  D  G  Q  F  R  Q  V  L  V  W    757

2341  GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG  2400
 758   R  D  L  D  N  P  R  S  L  A  L  D  P  T  K  G  Y  I  Y  W    777

2401  GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT  2460
 778   T  E  W  G  G  K  P  R  I  V  R  A  F  M  D  G  T  N  C  M    797

2461  GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG  2520
 798   T  L  V  D  K  V  G  R  A  N  D  L  T  I  D  Y  A  D  Q  R    817

2521  CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA  2580
 818   L  Y  W  T  D  L  D  T  N  M  I  E  S  S  N  M  L  G  Q  E    837

2581  GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA  2640
 838   R  V  V  I  A  D  D  L  P  H  P  F  G  L  T  Q  Y  S  D  Y    857

2641  TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG  2700
 858   I  Y  W  T  D  W  N  L  H  S  I  E  R  A  D  K  T  S  G  R    877

2701  GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC  2760
 878   N  R  T  L  I  Q  G  H  L  D  F  V  M  D  I  L  V  F  H  S    897
```

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FIG. 6F

```
2761  CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG  2820
 898   S  R  Q  D  G  L  N  D  C  M  H  N  N  G  Q  C  G  Q  L  C   917

2821  CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG  2880
 918   L  A  I  P  G  G  H  R  C  G  C  A  S  H  Y  T  L  D  P  S   937

2881  CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG  2940
 938   S  R  N  C  S  P  P  T  T  F  L  L  F  S  Q  K  S  A  I  S   957

2941  TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG  3000
 958   R  M  I  P  D  D  Q  H  S  P  D  L  I  L  P  L  H  G  L  R   977

3001  GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG  3060
 978   N  V  K  A  I  D  Y  D  P  L  D  K  F  I  Y  W  V  D  G  R   997

3061  CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG  3120
 998   Q  N  I  K  R  A  K  D  D  G  T  Q  P  F  V  L  T  S  L  S  1017

3121  CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC  3180
1018   Q  G  Q  N  P  D  R  Q  P  H  D  L  S  I  D  I  Y  S  R  T  1037

3181  ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC  3240
1038   L  F  W  T  C  E  A  T  N  T  I  N  V  H  R  L  S  G  E  A  1057

3241  CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA  3300
1058   M  G  V  V  L  R  G  D  R  D  K  P  R  A  I  V  V  N  A  E  1077
```

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FIG. 6G

```
3301  GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC   3360
1078   R  G  Y  L  Y  F  T  N  M  Q  D  R  A  A  K  I  E  R  A  A    1097

3361  CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT   3420
1098   L  D  G  T  E  R  E  V  L  F  T  T  G  L  I  R  P  V  A  L    1117

3421  GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA   3480
1118   V  V  D  N  T  L  G  K  L  F  W  V  D  A  D  L  K  R  I  E    1137

3481  GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC   3540
1138   S  C  D  L  S  G  A  N  R  L  T  L  E  D  A  N  I  V  Q  P    1157

3541  TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT   3600
1158   L  G  L  T  I  L  G  K  H  L  Y  W  I  D  R  Q  Q  Q  M  I    1177

3601  CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA   3660
1178   E  R  V  E  K  T  T  G  D  K  R  T  R  I  Q  G  R  V  A  H    1197

3661  CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG   3720
1198   L  T  G  I  H  A  V  E  E  V  S  L  E  E  F  S  A  H  P  C    1217

3721  TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG   3780
1218   A  R  D  N  G  G  C  S  H  I  C  I  A  K  G  D  G  T  P  R    1237

3781  GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC   3840
1238   C  S  C  P  V  H  L  V  L  L  Q  N  L  L  T  C  G  E  P  P    1257
```

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FIG. 6H

```
3841  CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC  3900
1258   T  C  S  P  D  Q  F  A  C  A  T  G  E  I  D  C  I  P  G  A   1277

3901  CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT  3960
1278   W  R  C  D  G  F  P  E  C  D  D  Q  S  D  E  E  G  C  P  V   1297

3961  GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG  4020
1298   C  S  A  A  Q  F  P  C  A  R  G  Q  C  V  D  L  R  L  R  C   1317

4021  CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT  4080
1318   D  G  E  A  D  C  Q  D  R  S  D  E  V  D  C  D  A  I  C  L   1337

4081  GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC  4140
1338   P  N  Q  F  R  C  A  S  G  Q  C  V  L  I  K  Q  Q  C  D  S   1357

4141  CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC  4200
1358   F  P  D  C  I  D  G  S  D  E  L  M  C  E  I  T  K  P  P  S   1377

4201  AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT  4260
1378   D  D  S  P  A  H  S  S  A  I  G  P  V  I  G  I  I  L  S  L   1397

4261  CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG  4320
1398   F  V  M  G  G  V  Y  F  V  C  Q  R  V  V  C  Q  R  Y  A  G   1417

4321  GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT  4380
1418   A  N  G  P  F  P  H  E  Y  V  S  G  T  P  H  V  P  L  N  F   1437
```

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FIG. 6I

```
4381  CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT   4440
1438   I  A  P  G  G  S  Q  H  G  P  F  T  G  I  A  C  G  K  S  M    1457

4441  GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA   4500
1458   M  S  S  V  S  L  M  G  G  R  G  G  V  P  L  Y  D  R  N  H    1477

4501  CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT   4560
1478   V  T  G  A  S  S  S  S  S  S  S  T  K  A  T  L  Y  P  P  I    1497

4561  CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA   4620
1498   L  N  P  P  P  S  P  A  T  D  P  S  L  Y  N  M  D  M  F  Y    1517

4621  CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC   4680
1518   S  S  N  I  P  A  T  A  R  P  Y  R  P  Y  I  I  R  G  M  A    1537

4681  GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG   4740
1538   P  P  T  T  P  C  S  T  D  V  C  D  S  D  Y  S  A  S  R  W    1557

4741  GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC   4800
1558   K  A  S  K  Y  Y  L  D  L  N  S  D  S  D  P  Y  P  P  P  P    1577

4801  CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA   4860
1578   T  P  H  S  Q  Y  L  S  A  E  D  S  C  P  P  S  P  A  T  E    1597

4861  GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC   4920
1598   R  S  Y  F  H  L  F  P  P  P  P  S  P  C  T  D  S  S         1615
```

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FIG. 6J

```
4921  TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA  4980
4981  AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA  5040
5041  TGTGAACTGTGATGGGGTGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT  5100
5101  AAACTTAATTTTGTAAAACA  5120
```

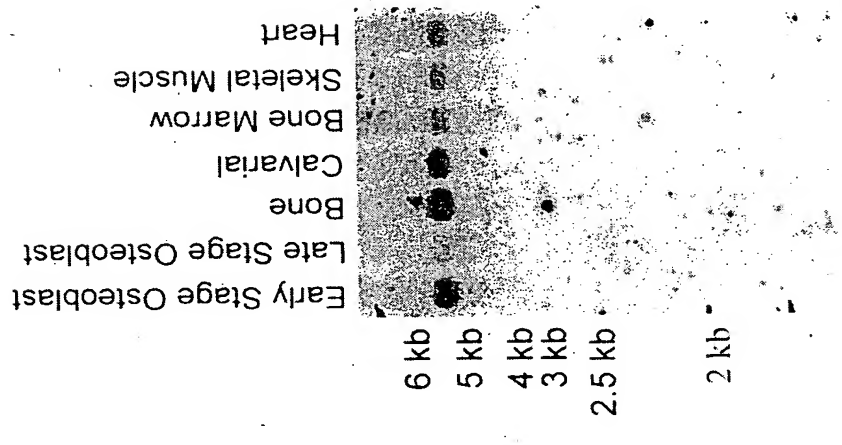

Early Stage Osteoblast
Late Stage Osteoblast
Bone
Calvarial
Bone Marrow
Skeletal Muscle
Heart
6 kb
5 kb
4 kb
3 kb
2.5 kb
2 kb
Northern Blot Analysis - Zmax 1

FIG. 7B

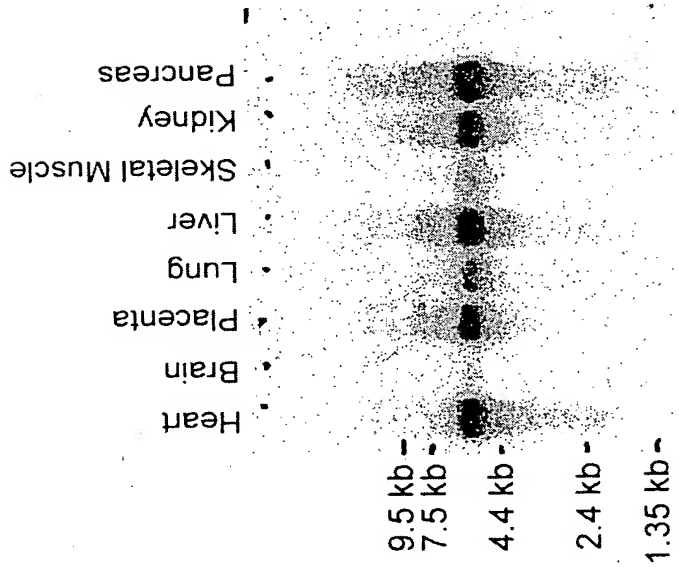

Heart
Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas
9.5 kb
7.5 kb
4.4 kb
2.4 kb
1.35 kb
Northern Blot Analysis - Zmax 1

FIG. 7A

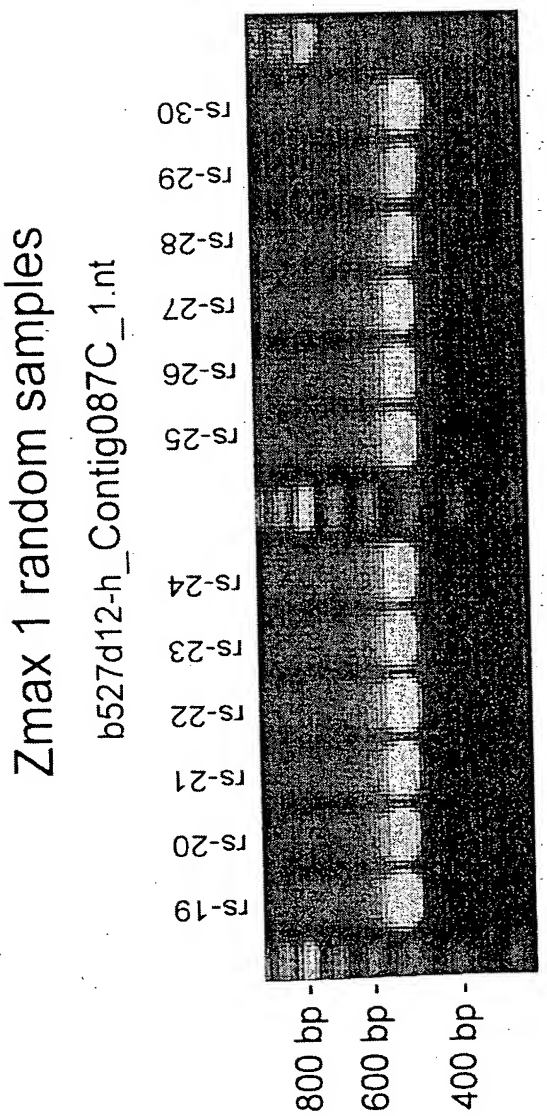

Zmax 1 random samples
b527d12-h_Contig087C_1.nt
rs-30
rs-29
rs-28
rs-27
rs-26
rs-25
rs-24
rs-23
rs-22
rs-21
rs-20
rs-19
800 bp -
600 bp -
400 bp -

FIG. 8

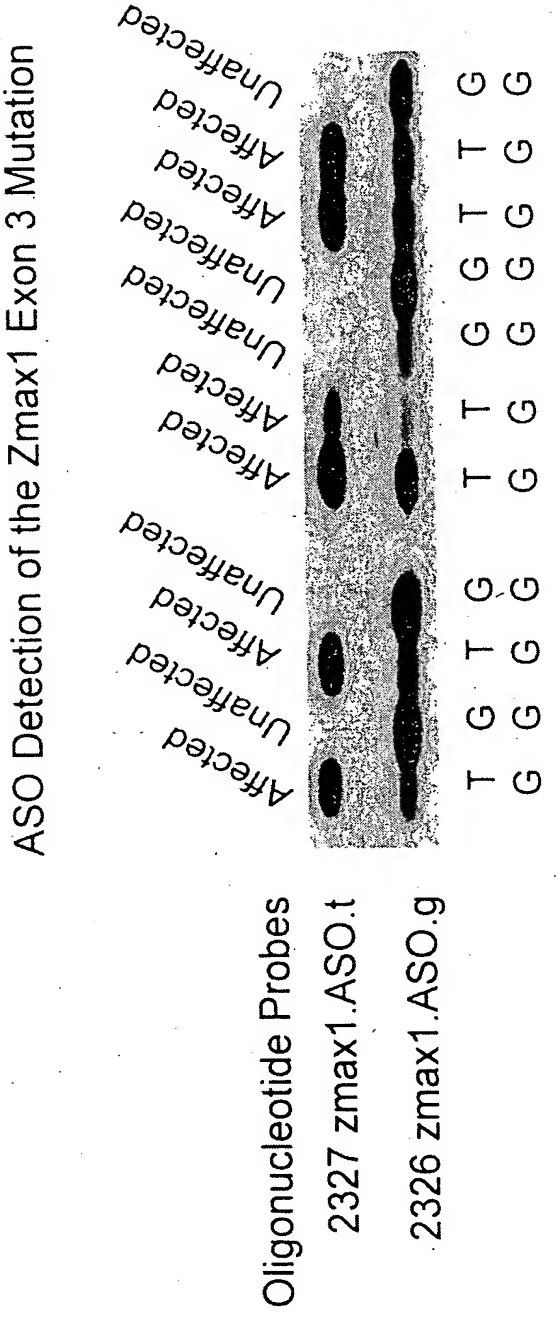

ASO Detection of the Zmax1 Exon 3 Mutation
Affected
Unaffected
Affected
Unaffected
Affected
Unaffected
Affected
Unaffected
Oligonucleotide Probes
2327 zmax1.ASO.t
2326 zmax1.ASO.g
T G T G T T G G T T G
G G G G G G G G G G
Genotype

FIG. 9

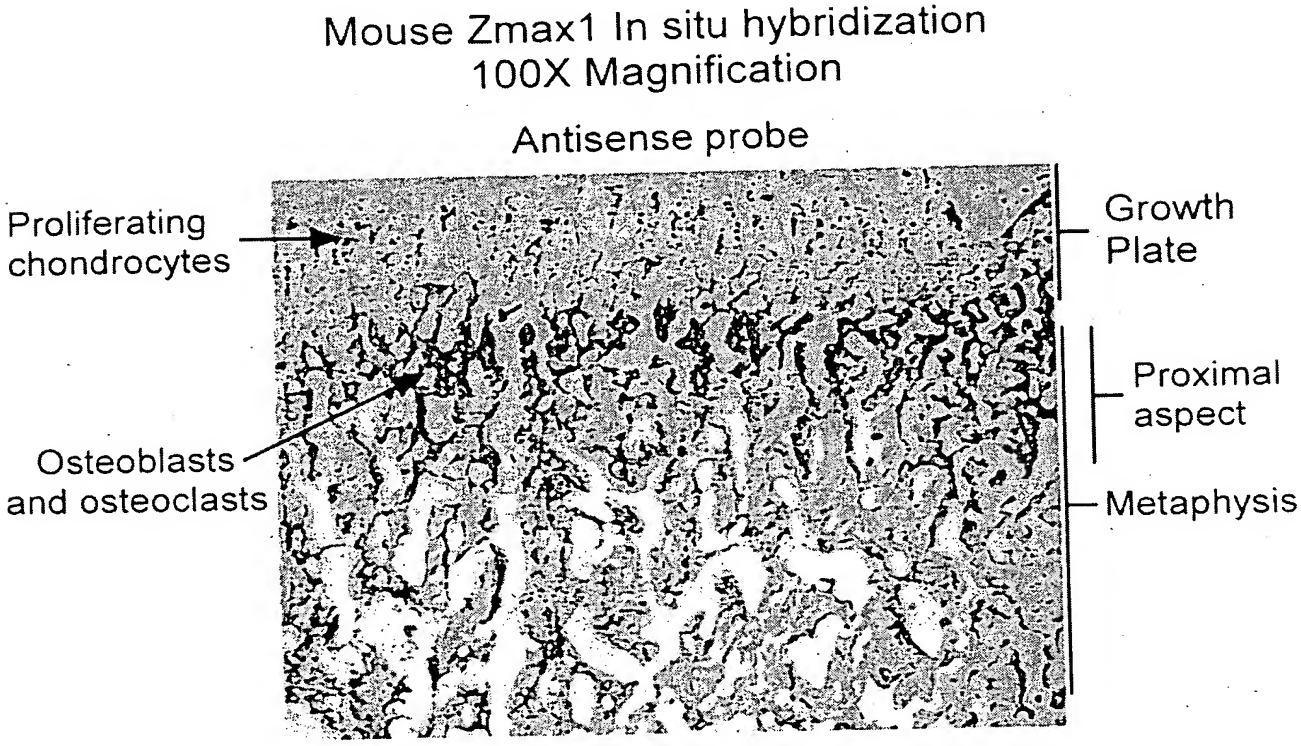


FIG. 10A

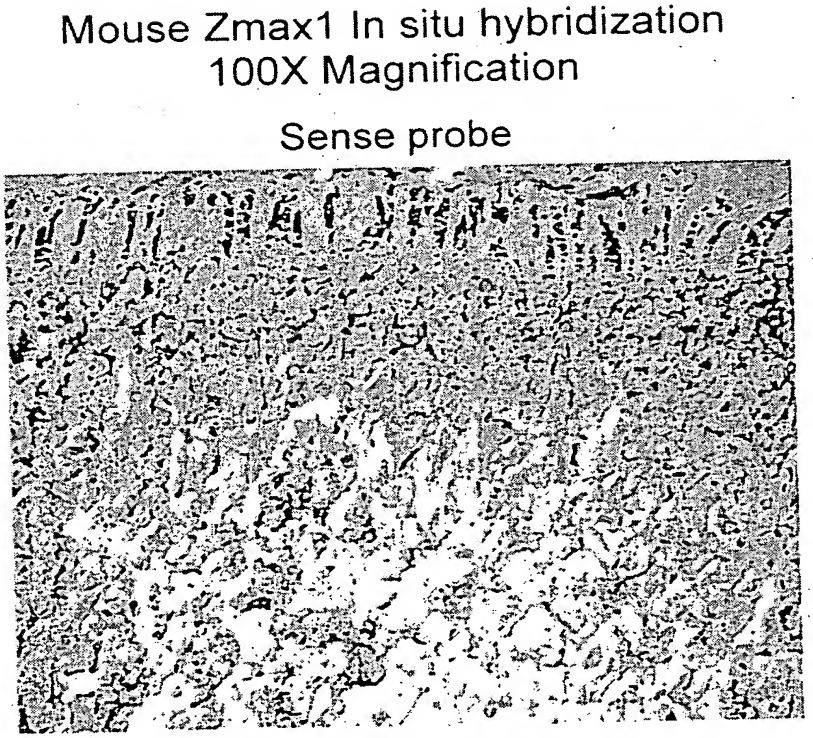


FIG. 10B

Mouse Zmax1 In situ hybridization
400X Magnification
Antisense probe

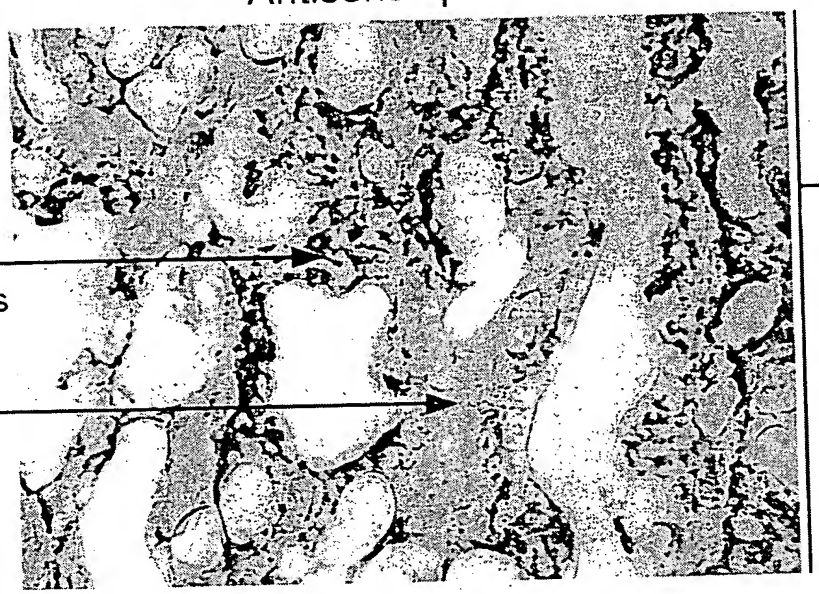


FIG. 11A

Mouse Zmax1 In situ hybridization
400X Magnification
Sense probe

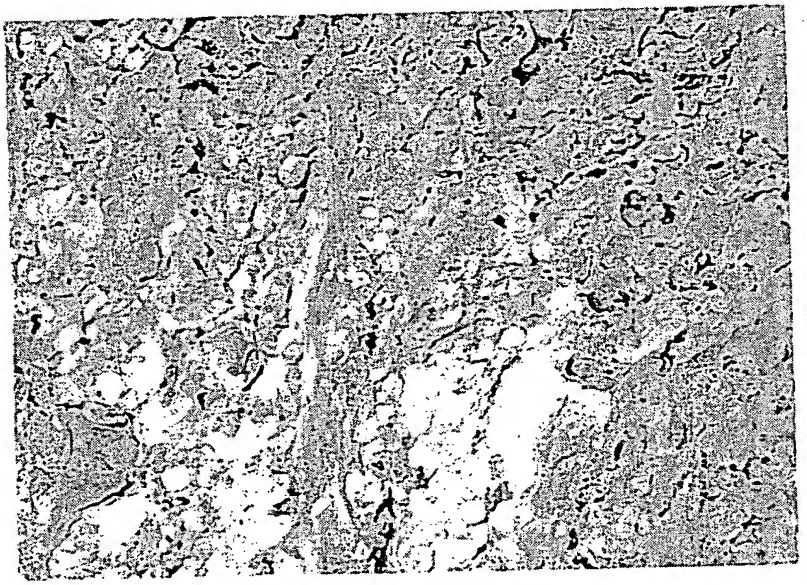


FIG. 11B

Mouse Zmax1 In situ hybridization
400X Magnification
Antisense probe

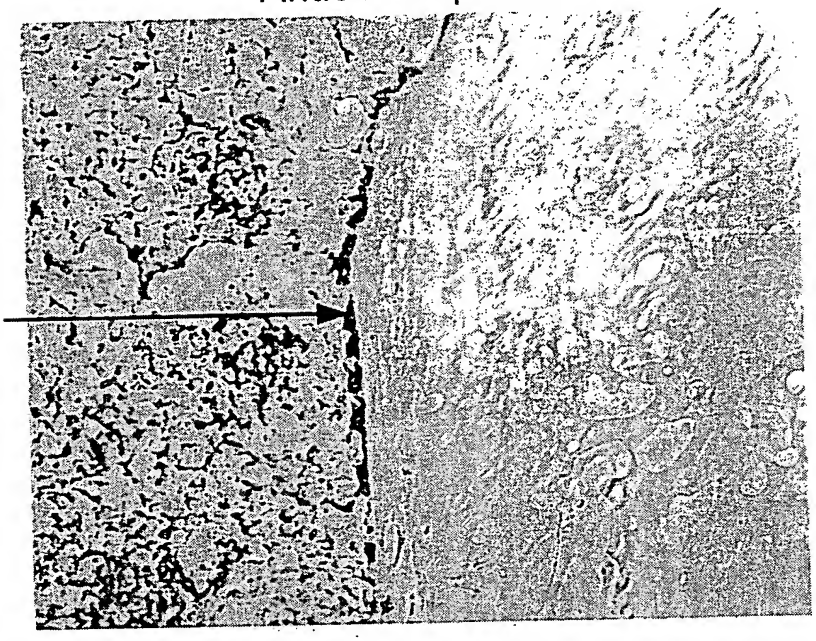


FIG. 12A

Mouse Zmax1 In situ hybridization
400X Magnification
Sense probe

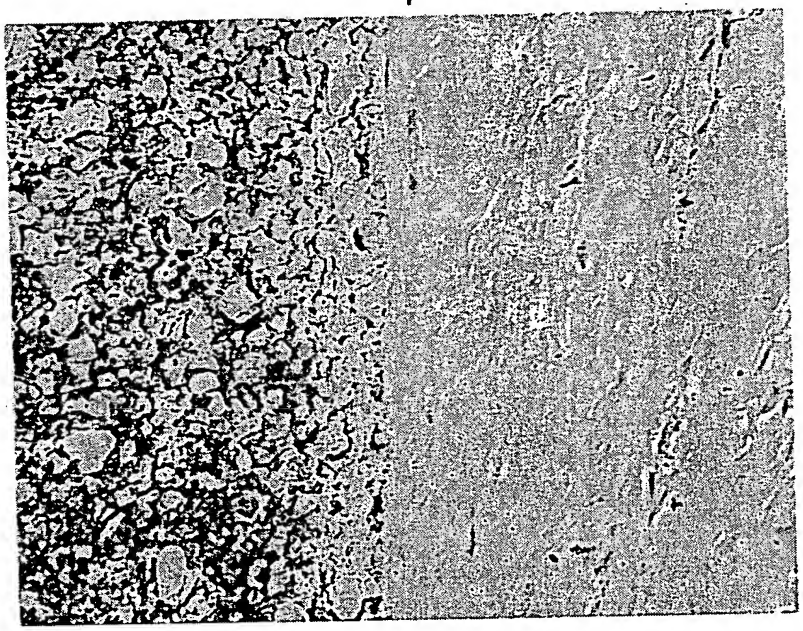
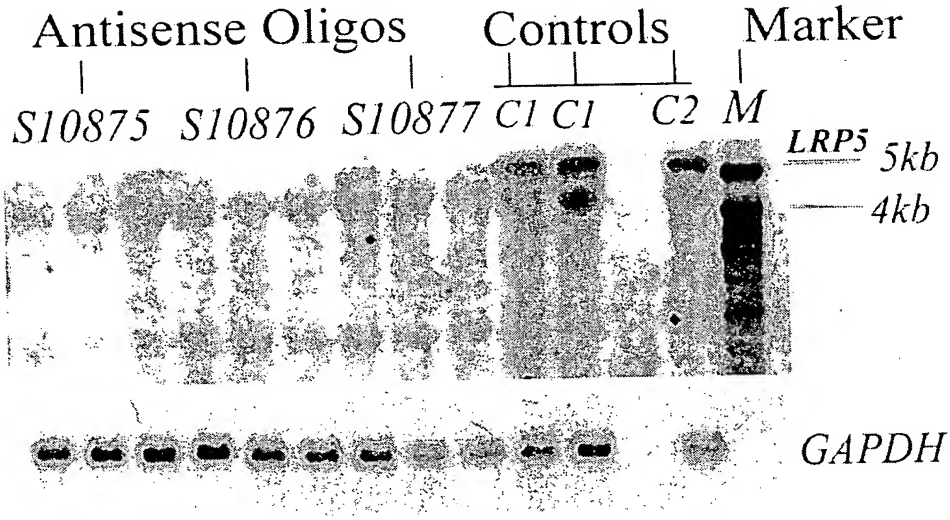


FIG. 12B

Antisense Inhibition of Zmax1 Expression



MC-3T3 cells

FIG. 13